

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/668936
Source: IFUO
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IFWO

RAW SEQUENCE LISTING

DATE: 11/30/2004

PATENT APPLICATION: US/10/668,936

TIME: 15:10:27

Input Set : N:\CrF3\RULE60\10668936.raw

Output Set: N:\CRF4\11302004\J668936.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: BIOGEN, INC.

7 (ii) TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
8 and Renal Growth

10 (iii) NUMBER OF SEQUENCES: 21

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Biogen, Inc.

14 (B) STREET: 14 Cambridge Center

15 (C) CITY: Cambridge

16 (D) STATE: MA

17 (E) COUNTRY: USA

18 (F) ZIP: 02142

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/10/668,936

C--> 28 (B) FILING DATE: 23-Sep-2003

C--> 34 (C) CLASSIFICATION:

C--> 51 (vii) PRIOR APPLICATION DATA:

W--> 32 (A) APPLICATION NUMBER: US 09/187,906

33 (B) FILING DATE: 06-NOV-1998

W--> 37 (A) APPLICATION NUMBER: PCT/US97/07726

38 (B) FILING DATE: 07-MAY-97

W--> 40 (A) APPLICATION NUMBER: US 60/017,427

41 (B) FILING DATE: 08-MAY-96

W--> 44 (A) APPLICATION NUMBER: US 60/019,300

45 (B) FILING DATE: 07-JUN-96

W--> 48 (A) APPLICATION NUMBER: US 60/021,859

49 (B) FILING DATE: 16-JUL-96

W--> 52 (A) APPLICATION NUMBER: US 60/043,533

53 (B) FILING DATE: 10-APR-97

C--> 55 (viii) ATTORNEY/AGENT INFORMATION:

56 (A) NAME: Kaplan, Warren A.

57 (B) REGISTRATION NUMBER: 34,199

58 (C) REFERENCE/DOCKET NUMBER: A008 PCT CIP

C--> 60 (ix) TELECOMMUNICATION INFORMATION:

61 (A) TELEPHONE: 617-679-2400

62 (B) TELEFAX: 617-679-2838

65 (2) INFORMATION FOR SEQ ID NO: 1:

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67      (i) SEQUENCE CHARACTERISTICS:
68          (A) LENGTH: 3616 base pairs
69          (B) TYPE: nucleic acid
70          (C) STRANDEDNESS: double
71          (D) TOPOLOGY: linear
73      (ii) MOLECULE TYPE: cDNA
75      (iii) HYPOTHETICAL: NO
77      (iv) ANTI-SENSE: NO
80      (ix) FEATURE:
81          (A) NAME/KEY: CDS
82          (B) LOCATION: 257..1660
85      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
87      GCGGCCGAG GTTGGGTCGG AACTGAACCC CTGAAAGCGG GTCCGCCTCC CGCCCTCGCG      60
89      CCCGCCGGA TCTGAGTCGC TGGCGGCGGT GGGCGGCAGA GCGACGGGGA GTCTGCTCTC      120
91      ACCCTGGATG GAGCTGAACT TTGAGTGGCC AGAGGAGCGC AGTCGCCCGG GGATCGCTGC      180
93      ACGCTGAGCT CTCTCCCCGA GACCGGGCGG CGGCTTTGGA TTTTGGGGGG GCGGGGACCA      240
95      GCTGCGCGGC GGCACC ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA      289
96          Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro
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99      CTC CTG GAT TTG CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG      337
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103      GAC TGT GTG AAA GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC      385
104      Asp Cys Val Lys Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser
105          30             35             40
107      ACC AAG TAC CGC ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC      433
108      Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn
109          45             50             55
111      TTC AGC CTG ACA TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC      481
112      Phe Ser Leu Thr Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala
113          60             65             70             75
115      ATG GAG GCC TTG AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG      529
116      Met Glu Ala Leu Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg
117          80             85             90
119      GGC ATG AAG AAA GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC      577
120      Gly Met Lys Lys Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr
121          95             100             105
123      CAG AGC CTG CAG GGA AAT GAC CTC CTG GAA GAT TCC CCG TAT GAG CCG      625
124      Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro
125          110             115             120
127      GTT AAC AGC AGG TTG TCA GAT ATA TTC CGG GCA GTC CCG TTC ATA TCA      673
128      Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser
129          125             130             135
131      GAT GTT TTC CAG CAA GTG GAA CAC ATT TCC AAA GGG AAC AAC TGC CTG      721
132      Asp Val Phe Gln Gln Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu
133          140             145             150             155
135      GAC GCA GCC AAG GCC TGC AAC CTG GAC GAC ACC TGT AAG AAG TAC AGG      769
136      Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg
137          160             165             170

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139	TCG GCC TAC ATC ACC CCC TGC ACC ACC AGC ATG TCC AAC GAG GTC TGC	817
140	Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys	
141	175 180 185	
143	AAC CGC CGT AAG TGC CAC AAG GCC CTC AGG CAG TTC TTC GAC AAG GTT	865
144	Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val	
145	190 195 200	
147	CCG GCC AAG CAC AGC TAC GGG ATG CTC TTC TGC TCC TGC CGG GAC ATC	913
148	Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile	
149	205 210 215	
151	GCC TGC ACC GAG CGG CGG CGA CAG ACT ATC GTC CCC GTG TGC TCC TAT	961
152	Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr	
153	220 225 230 235	
155	GAA GAA CGA GAG AGG CCC AAC TGC CTG AGT CTG CAA GAC TCC TGC AAG	1009
156	Glu Glu Arg Glu Arg Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys	
157	240 245 250	
159	ACC AAT TAC ATC TGC AGA TCT CGC CTT GCA GAT TTT TTT ACC AAC TGC	1057
160	Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys	
161	255 260 265	
163	CAG CCA GAG TCA AGG TCT GTC AGC AAC TGT CTT AAG GAG AAC TAC GCA	1105
164	Gln Pro Glu Ser Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala	
165	270 275 280	
167	GAC TGC CTC CTG GCC TAC TCG GGA CTG ATT GGC ACA GTC ATG ACT CCC	1153
168	Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro	
169	285 290 295	
171	AAC TAC GTA GAC TCC AGC AGC CTC AGC GTG GCA CCA TGG TGT GAC TGC	1201
172	Asn Tyr Val Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys	
173	300 305 310 315	
175	AGC AAC AGC GGC AAT GAC CTG GAA GAC TGC TTG AAA TTT CTG AAT TTT	1249
176	Ser Asn Ser Gly Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe	
177	320 325 330	
179	TTT AAG GAC AAT ACT TGT CTC AAA AAT GCA ATT CAA GCC TTT GGC AAT	1297
180	Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn	
181	335 340 345	
183	GGC TCA GAT GTG ACC ATG TGG CAG CCA GCC CCT CCA GTC CAG ACC ACC	1345
184	Gly Ser Asp Val Thr Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr	
185	350 355 360	
187	ACT GCC ACC ACT ACC ACT GCC TTC CGG GTC AAG AAC AAG CCT CTG GGG	1393
188	Thr Ala Thr Thr Thr Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly	
189	365 370 375	
191	CCA GCA GGG TCT GAG AAT GAG ATC CCC ACA CAC GTT TTA CCA CCC TGT	1441
192	Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys	
193	380 385 390 395	
195	GCG AAT TTG CAG GCT CAG AAG CTG AAA TCC AAT GTG TCG GGT AGC ACA	1489
196	Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr	
197	400 405 410	
199	CAC CTC TGT CTT TCT GAT AGT GAT TTC GGA AAG GAT GGT CTC GCT GGT	1537
200	His Leu Cys Leu Ser Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly	
201	415 420 425	
203	GCC TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCC AGC TGC	1585

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204   Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys
205           430           435           440
207   AGT CTG AGC TCA CTG CCG GTG CTG ATG CTC ACC GCC CTT GCT GCC CTG      1633
208   Ser Leu Ser Ser Leu Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu
209           445           450           455
211   TTA TCT GTA TCG TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA      1680
212   Leu Ser Val Ser Leu Ala Glu Thr Ser
213   460           465
215   GTATGAAAAG ACAAAGAGA ACCAAGTATT CTGTCCCTGT CCTCTTGAT ATCTGAAAAT      1740
217   CCAGTTTAA AAGCTCCGTT GAGAAGCAGT TTCACCCAAC TGGAACCTTT TCCTTGTTTT      1800
219   TAAGAAAGCT TGTGGCCCTC AGGGGCTTCT GTTGAAGAAC TGCTACAGGG CTAATTCCAA      1860
221   ACCCATAAGG CTCTGGGGCG TGGTGCGGCT TAAGGGGACC ATTTGCACCA TGTAAAGCAA      1920
223   GCTGGGCTTA TCATGTGTTT GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAATTTTA      1980
225   ACAGCTTGAA CCCTGTTCTC TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC      2040
227   TTCCATGTCT TACTCAGCAG CATTCGCCTT TGAAGACAGG CCCGCAGCCT AGTGTGAATG      2100
229   ACAAGTGGAG GTTGGCCTCA AGAGTGGACT TGGCAGACTC TACCTTGTA TAATGTTTAC      2160
231   CTTTCCGTGT ATGGTCTCCA CAGAGTGTTT ATGTATTTAC AGACTGTTCT GTGATCCCCC      2220
233   AACAACAACA ACCACAAATT CCTTGGTTCAC CTCCAAATGT AACCGTCCT TTAGCCAGT      2280
235   AGAGGAGGGT GGGTGTGGCC CTGGCACAGC TCCCGGATTG TTGATGGGCA CTCTCCTGAG      2340
237   CTTTGCTTGA GTGAGAAGCT GAATGTAGCT GAAAATCAAC TCTTCTTACA CTTCTTACTG      2400
239   CTTGCTTAC TTACGAGGTC ACATATAGAA CAAACATCAC CAACTATTAG CTTACCGTTA      2460
241   GCTTCCAAC TATTAGCTTT CTATGTTTTG AAAGCAGTGT TGCTGACCCC ATGTTTTAAT      2520
243   GATGGTTTAA TACATGCAGC CCTTTCCTCT CATCGGTAAC ACTAGCTCCA ACATCAACTT      2580
245   CATGCATGTG GCTCTCAAAA GCAGGCCCA AGAAGCCCAG TTCTTTAGGA GAAAGCTGCG      2640
247   TCCTGTTTCT GTGGACAGGC AGGAGGAAAC AGAGCAGCCT GCCCGTGGTG TCTTTATCTG      2700
249   TTTTGAAATC AAGGCTGCCT GTGTGTAAGG AATGGTTCAA TTCTTATAAA GGGTGCCACT      2760
251   GTTGATGCCA CAACTGGCAG TTGGTCTAGC TCCAGGACAC CGGTTTCCAT GTTGCCCTGGC      2820
253   AGAGACAGCT TTGATTGGGA CTGGCTGGCC ACAAGGGATG GGATGAAGAT GTGCTGCCCT      2880
255   CTCTTTCAAA GTTGAAGCCCT GCCAGGGCAC ATAGAAGCAT CTTTGCTCCT GACCACAACG      2940
257   TAGAACAGT TGGATTCAAG GTCATCAAGC GTCTCCTGTA CATTGCTCTG TGACCTTCAT      3000
259   AACAGCTGT CCCGACAAA AGGAACGGCA GTTTATGGAT CTAGAGTGGG AGCACAGGGT      3060
261   CTGGAAAGGT GAACCGATTG GCAAAATACA CAGAACAGGA GGGAGAGTCT CAAGCCGAGA      3120
263   CATCTTGCTT ACTAGCCACA CACCATCTCC TGGAGCCCTC CTCCTGACCT GGGCAGACCC      3180
265   TTAGGTGTAT ATCTAAAGAC CTCTTCAATG TTCAGGTTCA GAATCTGTAA ATGGTTGCGT      3240
267   CCTGGCACCC ATTCTGAAA ACTGAACAAA GGAGAGGATA TCTTTCCTCC ATTGAGCCCT      3300
269   GAAAGTATGA CTGGCTTCTC ACCCTCCCAC AGAGCAGGGA GCCCTGGTGC ACACAGTCTC      3360
271   CTGATATCCT CCCTGCTCTT TGAGGTTTGC CTTGGGAGAA AATGATTAC CTCGGGAGGG      3420
273   GACGCTTTGG TGTCTGAAGT ACGTTTATAT CGAAATGTTA ATGAATACCC ATGTAAAATA      3480
275   CTCAATAGCC ACCTTCTTTC CCTTCACAAT GTTTTCGAGG GGAATGCATC CAACATCCAA      3540
277   GTGTACCTGG TCAGTGGGAA GTTCCATGAA GACTCATACA TTGAATAAAC ATATTGATG      3600
279   TGCCGAAAGC GGCCGC      3616
282 (2) INFORMATION FOR SEQ ID NO: 2:
284   (i) SEQUENCE CHARACTERISTICS:
285       (A) LENGTH: 468 amino acids
286       (B) TYPE: amino acid
287       (D) TOPOLOGY: linear
289   (ii) MOLECULE TYPE: protein
291   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
293   Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu

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294      1          5          10          15
296 Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
297      20          25          30
299 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
300      35          40          45
302 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser
303      50          55          60
305 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
306      65          70          75          80
308 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
309      85          90          95
311 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
312      100          105          110
314 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
315      115          120          125
317 Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln
318      130          135          140
320 Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
321      145          150          155          160
323 Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
324      165          170          175
326 Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys
327      180          185          190
329 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
330      195          200          205
332 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
333      210          215          220
335 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg
336      225          230          235          240
338 Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
339      245          250          255
341 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
342      260          265          270
344 Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
345      275          280          285
347 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser
348      290          295          300
350 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
351      305          310          315          320
353 Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
354      325          330          335
356 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
357      340          345          350
359 Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
360      355          360          365
362 Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
363      370          375          380
365 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
366      385          390          395          400

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Input Set : N:\Crf3\RULE60\10668936.raw

Output Set: N:\CRF4\11302004\J668936.raw

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L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:31 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:34 M:220 C: Keyword misspelled or invalid format, [(C) CLASSIFICATION:]
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:34 M:220 C: Keyword misspelled or invalid format, Poss data loss, (C) CLASSIFICATION:
L:40 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)
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